Claims:

1. A method for whole genome amplification comprising:

(a) treating genomic DNA with a modifying agent which modifies cytosine bases but does not modify 5'-methyl-cytosine bases under conditions to form single stranded modified DNA;

(b) providing a population of random X-mers of exonuclease-resistant primers capable of binding to at least one strand of the modified DNA, wherein X is an integer 3 or greater;

(c) providing polymerase capable of amplifying double stranded DNA, together with nucleotides and optionally any suitable buffers or diluents to the modified DNA; and

(d) allowing the polymerase to amplify the modified DNA.

2. The method according to claim 1 wherein conditions used in step (a) do not result in substantial DNA fragmentation.

3. The method according to claim 1 or 2 wherein the modifying agent is selected from bisulphite, acetate or citrate.

4. The method according to claim 3 wherein the agent is sodium bisulphite.

5. The method according to any one of claims 1 to 4 wherein the exonuclease-resistant primers are oligonucleotides or oligonucleotide analogues containing at least one intercalator pseudonucleotide forming an intercalating nucleic acid (INA).

6. The method according to claim 5 wherein the oligonucleotide or oligonucleotide analogue is selected from the group consisting of subunits of DNA, RNA, peptide nucleic acid (PNA), hexitol nucleic acid (HNA), MNA, altritol nucleic acid (ANA), locked nucleic acid (LNA), cyclohexanyl nucleic acid (CAN), CeNA, TNA, (2'-NH)-TNA, nucleic acid based conjugates, (3'-NH)-TNA, α-L-Ribo-LNA, α-L-Xylo-LNA, β-D-Xylo-LNA, α-D-Ribo-LNA, [3.2.1]-LNA, Bicyclo-DNA, 6-Amino-Bicyclo-DNA, 5-epi-Bicyclo-DNA, α-Bicyclo-DNA, Tricyclo-DNA, Bicyclo[4.3.0]-DNA, Bicyclo[3.2.1]-DNA, Bicyclo[4.3.0]amide-DNA, β-D-Ribopyranosyl-NA, α-L-Lyxopyranosyl-NA, 2'-R-RNA, 2'-OR-RNA, α-L-RNA, and β-D-RNA.

7. The method according to claim 6 wherein the exonuclease-resistant primers are intercalating nucleic acids (INAs) formed from oligonucleotides.

8. The method according to any one of claims 1 to 7 wherein the primers are formed of two populations of INA primers, the first population being random X-mers containing the bases A, G and T, and the second population comprising random X-mers containing the bases A, C and T.

9. The method according to claim 8 wherein one population of primers is capable of binding to one strand of DNA while the other population of primers is capable of binding to a complimentary synthesized strand of the DNA stand to which the first population of primers bind.

10. The method according to claim 9 wherein the primers contain from 3 to 40 bases.

11. The method according to claim 10 wherein the primers contain about 6 to 20 bases.

12. The method according to any one of claims 1 to 11 wherein the polymerase is selected from phi29, or a modified version thereof, or a functional equivalent thereof capable of amplifying double stranded DNA *in vitro* without the need to denature the DNA.

13. The method according to claim 12 wherein the polymerase is phi29.

14. The method according to any one of claims 1 to 11 wherein the polymerase comprises a polymerase cocktail comprising a mixture of at least one proof-reading DNA polymerase and at least one non proof-reading DNA polymerase, wherein the ratio of proof-reading polymerase to non proof-reading polymerase is at least about 1:2.

15. The method according to claim 14 wherein the proof-reading DNA polymerase is selected from the group consisting of Pfu polymerase, Pfu polymerase turbo, Vent polymerase, Vent exo- polymerase, Pwo polymerase, $9°N_m$DNA polymerase, Therminator, *Pfx* DNA polymerase, Expand DNA polymerase, rTth DNA polymerase, and DyNAzyme EXT Polymerase.

16. The method according to claim 14 or 15 wherein the non proof-reading DNA polymerase is selected from the group consisting of Taq polymerase, Taq polymerase Stoffel fragment, Advantage DNA polymerase, AmpliTaq, Amplitaq Gold, Titanium Taq polymerase, KlenTaq DNA polymerase, Platinum Taq polymerase, and Accuprime Taq polymerase.

17. The method according to any one of claims 14 to 16 wherein the ratio of proof-reading polymerase to non-proof-reading polymerase is at least about 1:5.

18. The method according to claim 17, wherein the ratio of proof-reading polymerase to non-proof-reading polymerase about 1:10.

19. The method according to any one of claims 14 to 18 wherein step (d) is carried out by DNA thermal cycling.

20. A population of random X-mers of exonuclease-resistant primers capable of binding to at least one strand of the modified DNA in whole genome amplification, where X is an integer of 3 or greater.

21. The population of primers according to claim 20 wherein the exonuclease-resistant primers are intercalating nucleic acids (INAs) formed from oligonucleotides.

22. The population of primers according to claim 21 wherein the random primers are formed of two populations of INA primers, the first population being random X-mers containing the bases A, G and T, and the second population comprising random X-mers containing the bases A, C and T.

23. The population of primers according to claim 22 wherein one population of primers is capable of binding to one strand of DNA while the other population of primers is capable of binding to a complimentary synthesized strand of the DNA stand to which the first population of primers bind.

24. The population of primers according to claim 23 wherein the primers contain from 3 to 40 bases.

25. The population of primers according to claim 24 wherein the primers contain about 6 to 20 bases.

26. A kit containing a population of primers according to any one of claims 20 to 25 for use in whole genome amplification.

27. Use of a population of primers according to any one of claims 20 to 25 for whole genome amplification.

28. A kit containing a population of primers according to any one of claims 20 to 25, and a polymerase capable of amplifying double stranded DNA for use in whole genome amplification.

29. The kit according to claim 28 wherein the polymerase is polymerase is selected from phi29, or a modified version thereof, or a functional equivalent thereof capable of amplifying double stranded DNA *in vitro* without the need to denature the DNA; or polymerase cocktail comprising a mixture of at least one proof-reading DNA polymerase and at least one non proof-reading DNA polymerase.